



PCT10

#6

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/030,549

DATE: 06/04/2002
TIME: 14:58:20

Input Set : A:\Igsln_pct.app
Output Set: N:\CRF3\06042002\J030549.raw

ENTERED

3 <110> APPLICANT: SOLVAY PHARMACEUTICALS B.V.
 5 <120> TITLE OF INVENTION: Novel human G-protein coupled receptor
 7 <130> FILE REFERENCE: SPW99.04
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/030,549
 C--> 10 <141> CURRENT FILING DATE: 2002-04-26
 12 <160> NUMBER OF SEQ ID NOS: 18
 14 <170> SOFTWARE: PatentIn Ver. 2.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 1659
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Homo sapiens
 21 <220> FEATURE:
 22 <221> NAME/KEY: CDS
 23 <222> LOCATION: (36)..(1559)
 25 <400> SEQUENCE: 1
 26 gcctgcaacc tgtcycacgc cctctggctg ttgcc atg acg tcc acc tgc acc 53
 27 Met Thr Ser Thr Cys Thr
 28 1 5
 29 aac agc acg cgc gag agt aac agc agc cac acg tgc atg ccc ctc tcc 101
 30 Asn Ser Thr Arg Glu Ser Asn Ser Ser His Thr Cys Met Pro Leu Ser
 31 10 15 20
 32 aaa atg ccc atc agc ctg gcc cac ggc atc atc cgc tca acc gtg ctg 149
 33 Lys Met Pro Ile Ser Leu Ala His Gly Ile Ile Arg Ser Thr Val Leu
 34 25 30 35
 35 gtt atc ttc ctc gcc gcc tct ttc gtc ggc aac ata gtg ctg gcg cta 197
 36 Val Ile Phe Leu Ala Ala Ser Phe Val Gly Asn Ile Val Leu Ala Leu
 37 40 45 50
 38 42 gtg ttg cag cgc aag ccg cag ctg ctg cag gtg acc aac cgt ttt atc 245
 39 Val Leu Gln Arg Lys Pro Gln Leu Leu Gln Val Thr Asn Arg Phe Ile
 40 44 55 60 65 70
 41 46 ttc aac ctc ctc gtc acc gac ctg ctg cag att tcg ctc gtg gcc ccc 293
 42 Phe Asn Leu Leu Val Thr Asp Leu Leu Gln Ile Ser Leu Val Ala Pro
 43 48 75 80 85
 44 50 tgg gtg gtg gcc acc tct gtg cct ctc ttc tgg ccc ctc aac agc cac 341
 45 Trp Val Val Ala Thr Ser Val Pro Leu Phe Trp Pro Leu Asn Ser His
 46 52 90 95 100
 47 ttc tgc acg gcc ctg gtt agc ctc acc cac ctg ttc gcc ttc gcc agc 389
 48 Phe Cys Thr Ala Leu Val Ser Leu Thr His Leu Phe Ala Phe Ala Ser
 49 56 105 110 115
 50 58 gtc aac acc att gtc ttg gtg tca gtg gat cgc tac ttg tcc atc atc 437
 51 Val Asn Thr Ile Val Leu Val Ser Val Asp Arg Tyr Leu Ser Ile Ile
 52 60 120 125 130
 53 62 cac cct ctc tcc tac ccg tcc aag atg acc cag cgc cgc ggt tac ctg 485

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Input Set : A:\IgsIn_pct.app
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63	His Pro Leu Ser Tyr Pro Ser Lys Met Thr Gln Arg Arg Gly Tyr Leu		
64 135	140	145	150
66	ctc ctc tat ggc acc tgg att gtg gcc atc ctg cag agc act cct cca	533	
67	Leu Leu Tyr Gly Thr Trp Ile Val Ala Ile Leu Gln Ser Thr Pro Pro		
68	155	160	165
70	ctc tac ggc tgg ggc cag gct gcc ttt gat gag cgc aat gct ctc tgc	581	
71	Leu Tyr Gly Trp Gly Gln Ala Ala Phe Asp Glu Arg Asn Ala Leu Cys		
72	170	175	180
74	tcc atg atc tgg ggg gcc agc ccc agc tac act att ctc agc gtg gtg	629	
75	Ser Met Ile Trp Gly Ala Ser Pro Ser Tyr Thr Ile Leu Ser Val Val		
76	185	190	195
78	tcc ttc atc gtc att cca ctg att gtc atg att gcc tgc tac tcc gtg	677	
79	Ser Phe Ile Val Ile Pro Leu Ile Val Met Ile Ala Cys Tyr Ser Val		
80	200	205	210
82	gtg ttc tgt gca gcc cgg agg cag cat gct ctg ctg tac aat gtc aag	725	
83	Val Phe Cys Ala Ala Arg Arg Gln His Ala Leu Leu Tyr Asn Val Lys		
84 215	220	225	230
86	aga cac agc ttg gaa gtc cga gac tgt gtg gag aat gag gat	773	
87	Arg His Ser Leu Glu Val Arg Val Lys Asp Cys Val Glu Asn Glu Asp		
88	235	240	245
90	gaa gag gga gca gag aag aag gag gag ttc cag gat gag agt gag ttt	821	
91	Glu Glu Gly Ala Glu Lys Glu Glu Phe Gln Asp Glu Ser Glu Phe		
92	250	255	260
94	cgc cgc cag cat gaa ggt gag gtc aag gcc aag gag ggc aga atg gaa	869	
95	Arg Arg Gln His Glu Gly Glu Val Lys Ala Lys Glu Gly Arg Met Glu		
96	265	270	275
98	gcc aag gac ggc agc ctg aag gcc aag gaa gga agc acg ggg acc agt	917	
99	Ala Lys Asp Gly Ser Leu Lys Ala Lys Glu Gly Ser Thr Gly Thr Ser		
100	280	285	290
102	gag agt agt gta gag gcc agg ggc agc gag gag gtc aga gag agc agc	965	
103	Glu Ser Ser Val Glu Ala Arg Gly Ser Glu Glu Val Arg Glu Ser Ser		
104 295	300	305	310
106	acg gtg gcc agc gac ggc agc atg gag ggt aag gaa ggc agc acc aaa	1013	
107	Thr Val Ala Ser Asp Gly Ser Met Glu Gly Lys Glu Gly Ser Thr Lys		
108	315	320	325
110	gtt gag gag aac agc atg aag gca gac aag ggt cgc aca gag gtc aac	1061	
111	Val Glu Glu Asn Ser Met Lys Ala Asp Lys Gly Arg Thr Glu Val Asn		
112	330	335	340
114	cag tgc agc att gac ttg ggt gaa gat ggc atg gag ttt ggt gaa gac	1109	
115	Gln Cys Ser Ile Asp Leu Gly Glu Asp Gly Met Glu Phe Gly Glu Asp		
116	345	350	355
118	gac atc aat ttc agt gag gat gac gtc gag gca gtg aac atc ccg gag	1157	
119	Asp Ile Asn Phe Ser Glu Asp Asp Val Glu Ala Val Asn Ile Pro Glu		
120	360	365	370
122	agc ctc cca ccc agt cgt aac agc aac agc aac cct cct ctg ccc	1205	
123	Ser Leu Pro Pro Ser Arg Arg Asn Ser Asn Ser Asn Pro Pro Leu Pro		
124 375	380	385	390
126	agg tgc tac cag tgc aaa gct gct aaa gtg atc atc atc att ttc	1253	
127	Arg Cys Tyr Gln Cys Lys Ala Ala Lys Val Ile Phe Ile Ile Phe		

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Input Set : A:\Igsln_pct.app
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128	395	400	405	
130	tcc tat gtg cta tcc ctg ggg ccc tac tgc ttt tta gca gtc ctg gcc			1301
131	Ser Tyr Val Leu Ser Leu Gly Pro Tyr Cys Phe Leu Ala Val Leu Ala			
132	410	415	420	
134	gtg tgg gtg gat gtc gaa acc cag gta ccc cag tgg gtg atc acc ata			1349
135	Val Trp Val Asp Val Glu Thr Gln Val Pro Gln Trp Val Ile Thr Ile			
136	425	430	435	
138	atc atc tgg ctt ttc ttc ctg cag tgc atc cac ccc tat gtc tat			1397
139	Ile Ile Trp Leu Phe Phe Leu Gln Cys Cys Ile His Pro Tyr Val Tyr			
140	440	445	450	
142	ggc tac atg cac aag acc att aag aag gaa atc cag gac atg ctg aag			1445
143	Gly Tyr Met His Lys Thr Ile Lys Lys Glu Ile Gln Asp Met Leu Lys			
144	455	460	465	470
146	aag ttc ttc tgc aag gaa aag ccc ccg aaa gaa gat agc cac cca gac			1493
147	Lys Phe Phe Cys Lys Glu Lys Pro Pro Lys Glu Asp Ser His Pro Asp			
148	475	480	485	
150	ctg ccc gga aca gag ggt ggg act gaa ggc aag att gtc cct tcc tac			1541
151	Leu Pro Gly Thr Glu Gly Thr Glu Gly Lys Ile Val Pro Ser Tyr			
152	490	495	500	
154	gat tct gct act ttt cct tgaaggtagt tctaaggcaa accttgaaaa			1589
155	Asp Ser Ala Thr Phe Pro			
156	505			
158	tcagtcccttc agccacagct attttagagct ttaaaaactac caggttcaat cactggttat			1649
160	gctttctgtg			1659
163	<210> SEQ ID NO: 2			
164	<211> LENGTH: 508			
165	<212> TYPE: PRT			
166	<213> ORGANISM: Homo sapiens			
168	<400> SEQUENCE: 2			
169	Met Thr Ser Thr Cys Thr Asn Ser Thr Arg Glu Ser Asn Ser Ser His			
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172	Thr Cys Met Pro Leu Ser Lys Met Pro Ile Ser Leu Ala His Gly Ile			
173	20	25	30	
175	Ile Arg Ser Thr Val Leu Val Ile Phe Leu Ala Ala Ser Phe Val Gly			
176	35	40	45	
178	Asn Ile Val Leu Ala Leu Val Leu Gln Arg Lys Pro Gln Leu Leu Gln			
179	50	55	60	
181	Val Thr Asn Arg Phe Ile Phe Asn Leu Leu Val Thr Asp Leu Leu Gln			
182	65	70	75	80
184	Ile Ser Leu Val Ala Pro Trp Val Val Ala Thr Ser Val Pro Leu Phe			
185	85	90	95	
187	Trp Pro Leu Asn Ser His Phe Cys Thr Ala Leu Val Ser Leu Thr His			
188	100	105	110	
190	Leu Phe Ala Phe Ala Ser Val Asn Thr Ile Val Leu Val Ser Val Asp			
191	115	120	125	
193	Arg Tyr Leu Ser Ile Ile His Pro Leu Ser Tyr Pro Ser Lys Met Thr			
194	130	135	140	
196	Gln Arg Arg Gly Tyr Leu Leu Tyr Gly Thr Trp Ile Val Ala Ile			
197	145	150	155	160

RAW SEQUENCE LISTING
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Input Set : A:\Igsln_pct.app
Output Set: N:\CRF3\06042002\J030549.raw

199 Leu Gln Ser Thr Pro Pro Leu Tyr Gly Trp Gly Gln Ala Ala Phe Asp
 200 165 170 175
 202 Glu Arg Asn Ala Leu Cys Ser Met Ile Trp Gly Ala Ser Pro Ser Tyr
 203 180 185 190
 205 Thr Ile Leu Ser Val Val Ser Phe Ile Val Ile Pro Leu Ile Val Met
 206 195 200 205
 208 Ile Ala Cys Tyr Ser Val Val Phe Cys Ala Ala Arg Arg Gln His Ala
 209 210 215 220
 211 Leu Leu Tyr Asn Val Lys Arg His Ser Leu Glu Val Arg Val Lys Asp
 212 225 230 235 240
 214 Cys Val Glu Asn Glu Asp Glu Glu Gly Ala Glu Lys Lys Glu Glu Phe
 215 245 250 255
 217 Gln Asp Glu Ser Glu Phe Arg Arg Gln His Glu Gly Glu Val Lys Ala
 218 260 265 270
 220 Lys Glu Gly Arg Met Glu Ala Lys Asp Gly Ser Leu Lys Ala Lys Glu
 221 275 280 285
 223 Gly Ser Thr Gly Thr Ser Glu Ser Ser Val Glu Ala Arg Gly Ser Glu
 224 290 295 300
 226 Glu Val Arg Glu Ser Ser Thr Val Ala Ser Asp Gly Ser Met Glu Gly
 227 305 310 315 320
 229 Lys Glu Gly Ser Thr Lys Val Glu Glu Asn Ser Met Lys Ala Asp Lys
 230 325 330 335
 232 Gly Arg Thr Glu Val Asn Gln Cys Ser Ile Asp Leu Gly Glu Asp Gly
 233 340 345 350
 235 Met Glu Phe Gly Glu Asp Asp Ile Asn Phe Ser Glu Asp Asp Val Glu
 236 355 360 365
 238 Ala Val Asn Ile Pro Glu Ser Leu Pro Pro Ser Arg Arg Asn Ser Asn
 239 370 375 380
 241 Ser Asn Pro Pro Leu Pro Arg Cys Tyr Gln Cys Lys Ala Ala Lys Val
 242 385 390 395 400
 244 Ile Phe Ile Ile Ile Phe Ser Tyr Val Leu Ser Leu Gly Pro Tyr Cys
 245 405 410 415
 247 Phe Leu Ala Val Leu Ala Val Trp Val Asp Val Glu Thr Gln Val Pro
 248 420 425 430
 250 Gln Trp Val Ile Thr Ile Ile Trp Leu Phe Phe Leu Gln Cys Cys
 251 435 440 445
 253 Ile His Pro Tyr Val Tyr Gly Tyr Met His Lys Thr Ile Lys Lys Glu
 254 450 455 460
 256 Ile Gln Asp Met Leu Lys Lys Phe Phe Cys Lys Glu Lys Pro Pro Lys
 257 465 470 475 480
 259 Glu Asp Ser His Pro Asp Leu Pro Gly Thr Glu Gly Gly Thr Glu Gly
 260 485 490 495
 262 Lys Ile Val Pro Ser Tyr Asp Ser Ala Thr Phe Pro
 263 500 505
 267 <210> SEQ ID NO: 3
 268 <211> LENGTH: 27
 269 <212> TYPE: DNA
 270 <213> ORGANISM: Artificial Sequence
 272 <220> FEATURE:

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Input Set : A:\Igsln_pct.app
Output Set: N:\CRF3\06042002\J030549.raw

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273 <223> OTHER INFORMATION: Description of Artificial Sequence:Primer
275 <220> FEATURE:
276 <221> NAME/KEY: variation
277 <222> LOCATION: (19)
278 <223> OTHER INFORMATION: Degenerated primers
280 <220> FEATURE:
281 <221> NAME/KEY: variation
282 <222> LOCATION: (22)
283 <223> OTHER INFORMATION: Degenerated primers
285 <220> FEATURE:
286 <221> NAME/KEY: variation
287 <222> LOCATION: (25)
288 <223> OTHER INFORMATION: Degenerated primers
290 <400> SEQUENCE: 3
W--> 291 catcttcgtc gtccggcacng ynggnaa 27
294 <210> SEQ ID NO: 4
295 <211> LENGTH: 26
296 <212> TYPE: DNA
297 <213> ORGANISM: Artificial Sequence
299 <220> FEATURE:
300 <223> OTHER INFORMATION: Description of Artificial Sequence:Primer
302 <220> FEATURE:
303 <221> NAME/KEY: variation
304 <222> LOCATION: (21)
305 <223> OTHER INFORMATION: Degenerated primers
307 <400> SEQUENCE: 4
W--> 308 gggtgtggcaga tggccarrya nckytc 26
311 <210> SEQ ID NO: 5
312 <211> LENGTH: 27
313 <212> TYPE: DNA
314 <213> ORGANISM: Artificial Sequence
316 <220> FEATURE:
317 <223> OTHER INFORMATION: Description of Artificial Sequence:Primer
319 <220> FEATURE:
320 <221> NAME/KEY: misc_feature
321 <222> LOCATION: (27)
322 <223> OTHER INFORMATION: Modified base : 3'-deoxyadenosine
324 <400> SEQUENCE: 5
325 acgggtggca acacgtgtac ggcgtta 27
328 <210> SEQ ID NO: 6
329 <211> LENGTH: 27
330 <212> TYPE: DNA
331 <213> ORGANISM: Artificial Sequence
333 <220> FEATURE:
334 <223> OTHER INFORMATION: Description of Artificial Sequence:Primer
336 <400> SEQUENCE: 6
337 ccatcctaattt acgactcaat atagggc 27
340 <210> SEQ ID NO: 7
341 <211> LENGTH: 23

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/030,549

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TIME: 14:58:22

Input Set : A:\Igsln_pct.app
Output Set: N:\CRF3\06042002\J030549.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 19,22,25

Seq#:4; N Pos. 21